

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC

119 TTCCCTTCACTACAAACTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC

239 TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTTATGCACAGGGTGGAACAAG

299 99 ATGGATTATCAAGTCTAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC S Ω

FIG. 1A-1

39 (UPPER: SEQ ID NO.: 1) 19 (LOWER: SEQ ID NO.: 4)

1/20

179 59 79

| 359 | 419 139 | 479 159 | 539 179 | 599 199 | 659 219 | 719 239 | 779 | |
|---|---|---|--|---|--|---|---|--------------------------|
| CAAAAAATCAATGIGAAGCAAATCGCCAGCCCGCCTCCGCTCTACTCACTGGTG Q K I N V K Q I A A R L L P P L Y S L V | TTCATCTTTGGTTTTGTGGGGAACATGCTGGTCATCCTCATCTTGATAAACTGCAAAAGG FIFGFVGNMLVILLILINCKR | CTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT L K S M T D I Y L L N L A I S D L F F L | CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCCCCAGTGGGACTTTGGAAATACAATG L T V P F W A H Y A A A Q W D F G N T M | TGTCAACTCTTGACAGGGCTCTATTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC C Q L L T G L Y F I G F F S G I F F I I | CTCCTGACAATCGATAGGTACCTGGCTGTCCATGCTGTTTGCTTTAAAAGCCAGG L L T I D R Y L A V H A V F A L K A R | ACGGTCACCTTTGGGGGGGGGGGGGGGGGGGGGGGGGGG | CTCCCAGGAATCATCTTACCAGATCTCAAAAAAAAGAAGGTCTTCATTACACCTGCAGCTCT L P G I I F T R S Q K E G L H Y T C S S | FIG 14.2 |
| AGC. | TGG(V (| ACA: | , GGG(₩ | 66CJ G | GGT7 | TGG1 | TTAC F 1 | |
| rgrg, v | l'TTG F | BACTG T | TTCI | acag T | GATA D | | ATCT I | 4 |
| CAA: N | 16G 6 | CAT(M | ည် | CITIC | AATC I | TTT | ATC | CATTTTCCATACA H F P Y |
| AAT | CTT | 3AG S | rgt(v | ACT L | AC. T | JAC(| 1997 1997 | CCAT |
| AAA. K | AT(I | AAC K | 'AC' | CAA | D I | GTC V | CCA | ATTTT H |
| E O O | TIC | CIG | CII | IGI C | CTC | ACG T | CIC | CAT |

| 299 | ATGGATTATCAAGTCTAATCTATGACATCAATTATTATACATCGGAGCCCTGC M D Y Q V S S P I Y D I N Y Y T S E P C |
|---|--|
| 239 79 | TAAATACATTCTAGGACTTTATAAAGATCACTTTTTTATTTA |
| 179 59 | CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC |
| 3/20 339 | TTCCCTTCACTACAAACTTCATTGCCTTGGCCAAAAGAGAGTTAATTCAATGTAGACAT |
| 59 (UPPER: SEQ ID NO.: 2) 19 (LOWER: SEQ ID NO.: 5 | GAATICUUU AAUAGAGUUAAGUTUTUU AATUTAGTGGAAGGAAGUTAGCAGCAAACU |

FIG. 1B-1

| | | | | | | | | LL. |
|--|---|---|--|--|---|---|---|---|
| 359 | 419 | 479 159 | 539 179 | 599 199 | 659 | 719 239 | 779 259 | 839 |
| CAAAAATCAATGTGAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG Q K I N V K Q I A A R L L P P L Y S L V | TTCATCTTTGGTTTTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG FIFGFVGNMLVILILILINCKRR | CTGAAGAGCATGACTGACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT L K S M T D I Y L L N L A I S D L F F L | CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCCCCAGTGGGACTTTGGAAATACAATG L T V P F W A H Y A A A Q W D F G N T M | TGTCAACTCTTGACAGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC CQLLTGKFIGFFSGIFFII | CTCCTGACAATCGATAGGTACCTGGCTGTCCATGCTGTTTTGCTTTAAAAGCCAGG L L T I D R Y L A V V H A V F A L K A R | ACGGTCACCTTTGGGGTGGTGACAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT TVTFGVVTFA | CTCCCAGGAATCATTTACCAGATCTCAAAAAAAAGAGGTCTTCATTACACCTGCAGCTCT L P G I I F T R S Q K E G L H Y T C S S | CATTTTCCATACAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC H F P Y S Q Y Q F W K N F Q T L K I V I |
| | | | | | | | | |

| TIGGGGCTGGTCCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACT L G L V L P L L V M V I C Y S G T 1. K T | 8 9 9 9 9 |
|--|-----------------------|
| CTGCTTCGGTGTCGAAAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC | 2 60 c |
| ATGATTGITTATTTTCTCTGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC M I V Y F L F W A P Y N I V L L L N T F | 1019 339 |
| CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG | 1079 |
| GTGACAGAGACTCTTGGGATGACGCACCTCATCATCTATGCCTTTGTC V T E T L G M T H C C I N P I I Y A F V | 1139 |
| GGGGAGAAGTTCAGAAACTACCTCTTCTTCCAAAAGCACATTGCCAAACGCTTC G E K F R N Y L L V F F Q K H I A K R F | 1199 |
| TGCAAATGCTGTTCTATTTTCCAGCAAGGCTCCGAGCGAG | 1259 |
| CGATCCACTGGGGAGCAGGAATATCTGTGGGCTTGTGACACGGGCTGGGTGGG | 1319 |
| GACCCAGTCAGAGTTGTGCACATGGCTTAGTTTTCATACACAGCCTGGGGCTGGGGGTNGG | 1379 |
| TIGGNNGAGGICTITITAAAAGGAAGTTACTGTTATAGAGGGTCTAAGATTCATCCATT | 1439 |
| TATITIGGCATCTGTTTAAAGTAGTAGATTAGATTAGATT | ` |

| GAATICCCCAAGGAAGCTAGCAAACCTAGAAAGCTAGCAAAACC | 59 (UPPER: SEQ ID NO. 3) 19 (LOWER: SEQ ID NO. 6) |
|--|--|
| TTCCCTTCACTACAAACTTCATTGCCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT | 119 39 |
| CTATGTAGGCAATTAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC | 179 59 |
| TAAATACATTCTAGGACTTTATAAAGATCACTTTTTTATGCACAGGGTGGAACAAG | 239 79 |
| ATGGATTATCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC M D Y Q V S S P I Y D I N Y Y T S E P C | 299 99 |

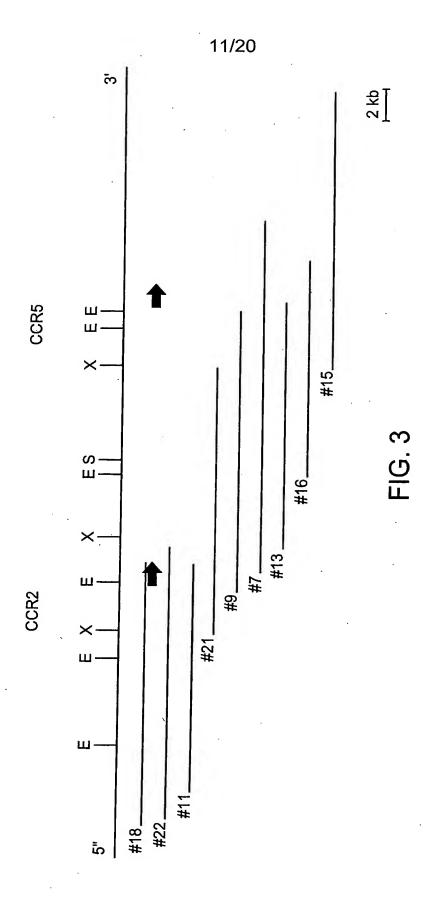
| 359 | 419 139 | 479 159 | 539 179 | 199 199 | 659 219 | 719 | 779 259 | 839 |
|--|--|--|---|--|--|--|---|--|
| CAAAAATCAATGTGAAGTGGCAGCCGCCTCCTGCCTCCGCTCTACTCACTGGTG | TTCATCTTTGGGTAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG | CTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT | CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCCCCAGTGGGACTTTGGAAATACAATG | TGTCAACTCTTGACAGGCTCTATTTATAGGCTTCTTCTGGAATCTTCTTCATCATC | CTCCTGACAATCGATAGGTACCTGGCTGTCTGTGTTTGCTTTAAAAGCCAGG | ACGGTCACCTTTGGGGGGGGACAAGTGTGACTTGGGTGGTGGCTGTGTTTGCGTCT | CTCCCAGGAATCATCTTACCAGATCTCAAAAAAAAAAAGAAGGTCTTCATTACACCTGCAGCTCT | CATTITCCATACATTAAGATAGTCATCTTGGGGCTGGTCCTGCCTG |
| Q K I N V K Q I A A R L L P P L Y S L V | FIFGFVGRMLVILLINCKR | L K S M T D I Y L L N L A I S D L F F L | L T V P F W A H Y A A A Q W D F G N T M | CQLLTGLYFIGFFSGIFFII | L L T I D R Y L A V V H A V F A L K A R | T V T F G V V T S V I T W V V A V F A S | L P G I I F T R S Q K E G L H Y T C S S | |

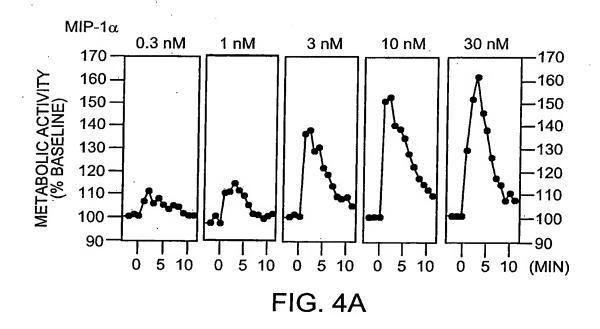
| CATCTGCTACTCGGAATCCTAAAACTCTGCTTCGGTGTCGAAATGAGAAGAGGCA H L L L G N P K N S A S V S K * | 899 299 | |
|--|-------------|--|
| CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTTATTTTCTCTTCTGGGCTCCCTA | 959 | |
| CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG | 1019 | |
| CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG | 1079 | |
| CATCAACCCCATCATGTTGTTGGGGGGGAGAAGTTCAGAAACTACCTCTTAGTCTT | 1139 | |
| CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTTTTTCCAGCAAGAGGC | 1199 | |
| TCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG | 1259 419 | |
| CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT | 1319 | |
| TTCATACACAGCCTGGGGGTNGGTTGGNNGAGGTCTTTTTAAAAGGAAGTTACT | 1379 459 | |
| GTTATAGAGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC | 1439 479 | |
| GAATTC | | |

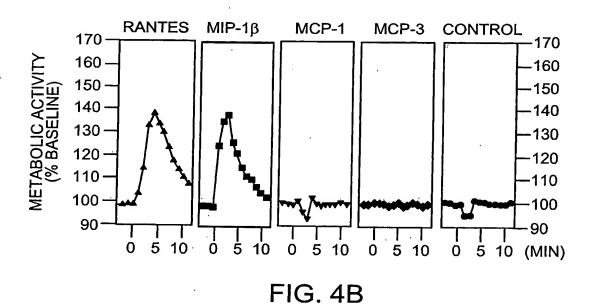
| 83 95 | 87 | 95 | 177 | 182 | 182 | 186 | 9/20 |
|------------|--|---|------|-----|---|---|---------|
| 6 MLSTSRSR | hcc-r3 hcc-r1 metpatteedygdatpcokWneragaqlippixsivrvigityvyyvyyvyyvyyvysisikNmtsixilnlaisdilfilf | ncc-r4 MNPTDIADTTLDESIYSNYKLYESIPKPCTKRGTKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKKKRLRSMTDVKLLNLAISDILFFVFS TTT | | Н : | NCC-RI LPFWIDYKLKDDWWFGDAMCKIHSGFYYTGLYSEFFFILLTIDRYLA IVHAVFALRARTVTFGVITSITIMALATIASMPGLYFSKTQWEFTR | TETIOTETH CHARLES WITH A STANDED BY THE STANDED BY | FIG. 2A |

| IA | IN ILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLINTFQEFFGLNNG 272 RNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRIVI FTIMIVYFLFWTPYNIVILLNTFQEFFGLISNC 280 MTJFGLVLPLLVMAICYNGITHKTLLRQPSKK, YRAHRLIFVIMAVFFIFWTPYNVAILLISSYGSILFGNDG 276 INLEGLVLPLLVMILCYNGITHKILLRRPNEKK, SKAVRLIFVIMITFFLFWTPYNLTILISSYGDFLFTHEC 276 INLIGLVIPLGTMLFCYSMITRTLQHQKNEKK, NKAVKMEFAVVVLFLGFWTPYNIVLFHETLVFLGFUDDG 279 | CCSIFQQEAPERASSVYTRSTGEQEISNGI 352 QCPVEYRETVDGVTSTNIPSTGEQENSAGL 360 XYIPFIPSTARTSSV.SPSTABEPELSIVF 355 XWIPFISVDRIERVSST.SPSTGEHEUSAGF 355 2YCGILQIYSADTPSSSYTQSTMDHDLHDAL 360 |
|----|---|---|
| | YTCSSHFPYSQYQFWKNFQTLKIJVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNG 272 KMCGPYFPRGWNNFHFITIMRNILGLVLPLLIJMVICYSGILKTLLRCRNEKKRHRAVRIVIFTIMIVYFLFWTPYNIVJILLNTFQEFFGLISNG 280 TLCSALYPEDTVYSWRHFHITLRMTJFGLVLPLLVMAICYHGIJTKTLLRCPSKK, YKALTRLIFVIMAVFFIJFWTPYNVAILLISSYQSILFGNJC 276 HTCSLHFPHESLREWKLFGALVLLFGLVLPLLVMILCYHGIJTKTLLRRPNEKK, SKAVRLIFVIMITFFLFWTPYNLTILLISVFQDFLFTHEC 276 TYCKTKYSLNST.TWKVLSSLEINTLGLVJPLGJMLFCYSMIJTRTLQHGKNEKK, NKAVKMLFAVVVLFLGFWTPYNIVLFLETLVELETLVELEVILQDC 279 | SSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKR.FCKGCSIFQQEAPERASSVYTRSTGEQEISVGL 352 ESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRNYLSVFFRKHIMKR.FCKQCPVFYRFTVDGVTSTNIJPSTGEQEVSAGL 360 ERSKHLDLVMIVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFHRHLLMH.LGRYIPFLPSAKLERTSSV.SPSTABEPELSIVF 355 EQSRHLDLAMQVTEVIAYTHCCVNPVIYAFVGERFRKYLRQLFHRRVAVH.LVKWLPFLSVDRLERVSST.SPSTGEHELSAGF 355 TFERYLDLAMQVTEVIAYHCCLNPIIYAFUGERFRKKYITLQLFHRRVAVH.LVKWLPFLSVDRLERVSSTROSTMDHDLHDAL 360 |
| | ccR5 hcc-R2b hcc-R3 hcc-R1 hcc-R4 | ccr5 hcc-r2b hcc-r3 hcc-r1 |

FIG. 2B







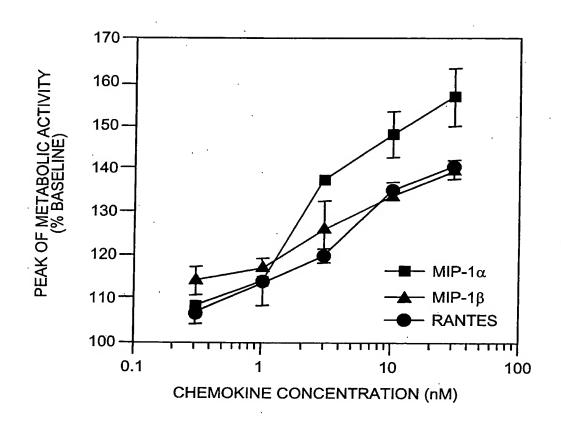


FIG. 4C

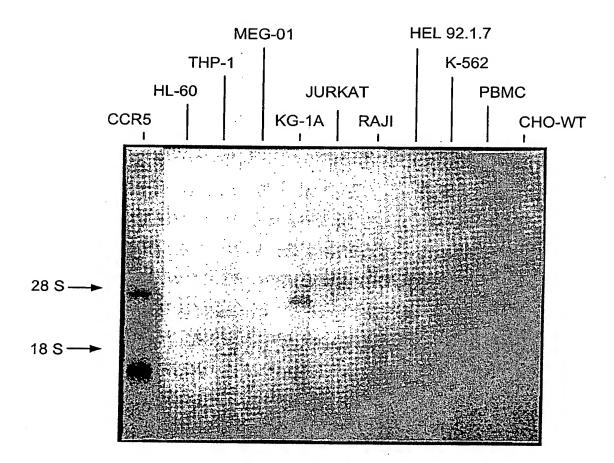
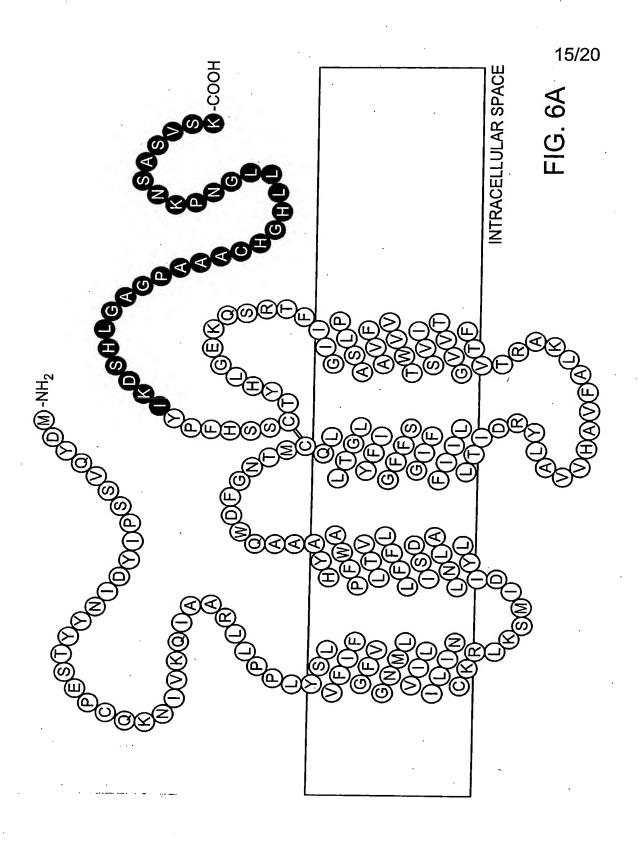
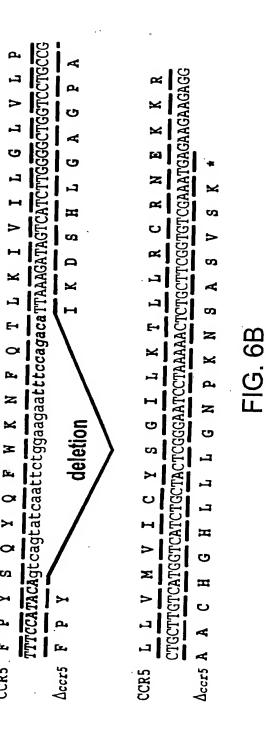
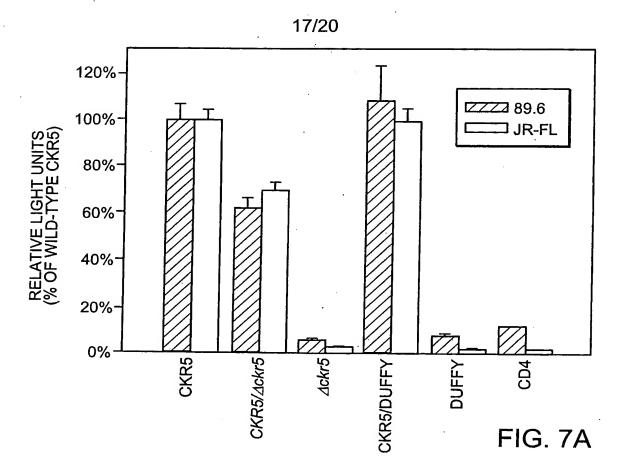
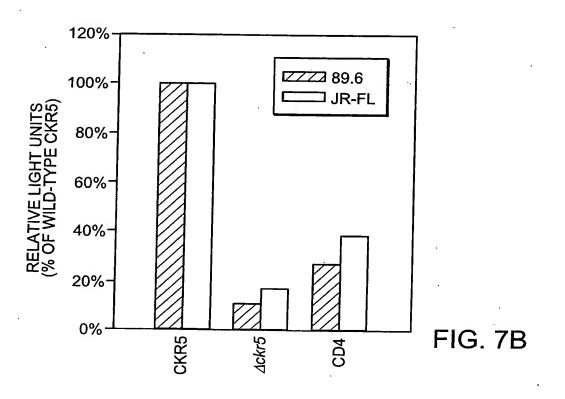


FIG. 5









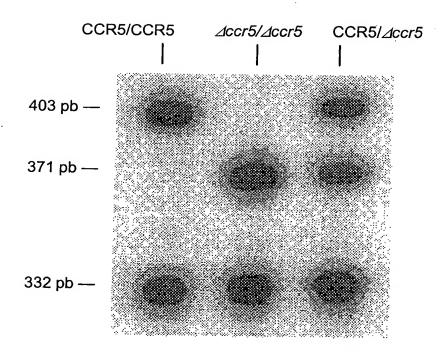
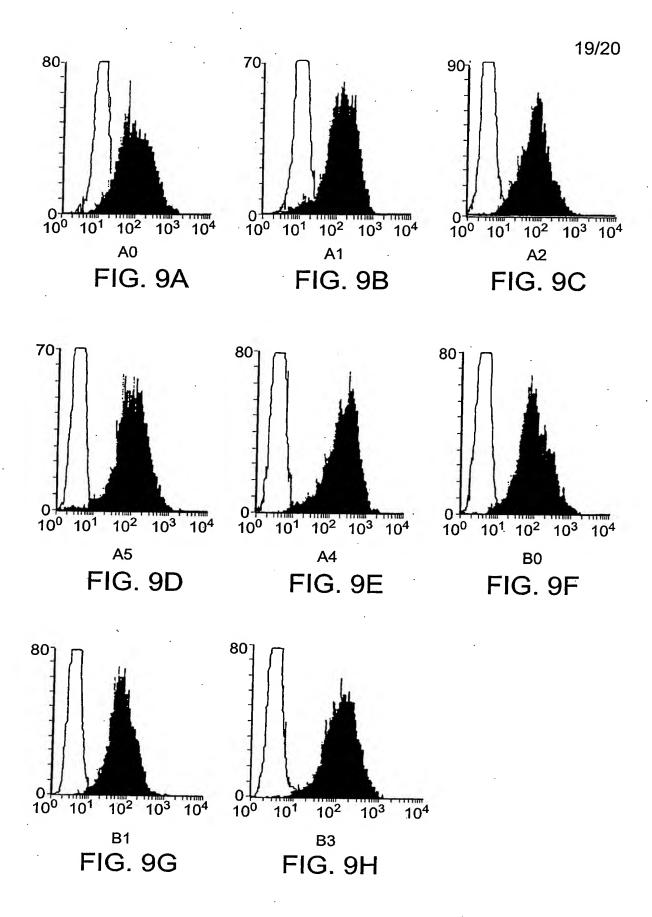


FIG. 8



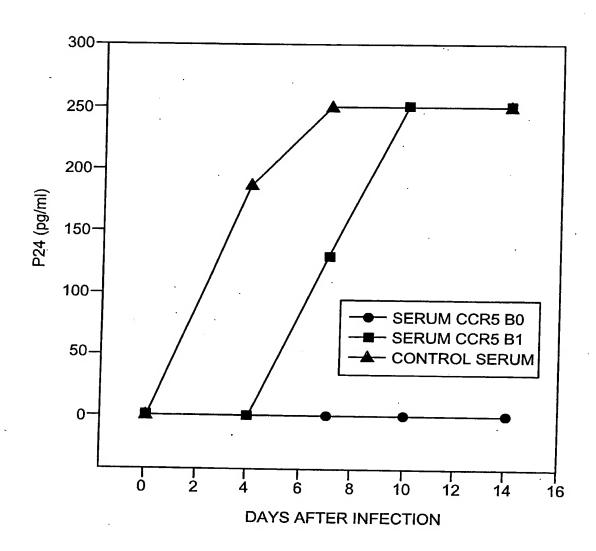


FIG. 10